ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA 50
M A L E Q N Q S T D Y Y Y E E N E

AATGAATGGC ACTTATGACT ACAGTCAATA TGAACTGATC TGTATCAAAG 100
M N G T Y D Y S Q Y E L I C I K E

AAGATGTCAG AGAATTTGCA AAAGTTTTCC TCCCTGTATT CCTCACAATA 150
D V R E F A K V F L P V F L T I

GTTTTCGTCA TTGGACTTGC AGGCAATTCC ATGGTAGTGG CAATTTATGC 200
V F V I G L A G N S M V V A I Y A

CTATTACAAG AAACAGAGAA CCAAAACAGA TGTGTACATC CTGAATTTGG 250
Y Y K K Q R T K T D V Y I L N L A

CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTTG GGCTGTTAAT 300
V A D L L L L F T L P F W A V N

GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC 350
A V H G W V L G K I M C K I T S A

CTTGTACACA CTAAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA 400
L Y T L N F V S G M Q F L A C I S

GCATAGACAG ATATGTGGCA GTAACTAAAG TCCCCAGCCA ATCAGGAGTG 450
I D R Y V A V T K V P S Q S G V

GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT 500
G K P C W I I C F C V W M A A I L

GCTGAGCATA CCCCAGCTGG TTTTTTATAC AGTAAATGAC AATGCTAGGT 550
L S I P Q L V F Y T V N D N A R C

GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT 600
I P I F P R Y L G T S M K A L I

CAAATGCTAG AGATCTGCAT TGGATTTGTA GTACCCTTTC TTATTATGGG 650
Q M L E I C I G F V V P F L I M G

GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA 700
V C Y F I T A R T L M K M P N I K

AAATATCTCG ACCCCTAAAA GTTCTGCTCA CAGTCGTTAT AGTTTTCATT 750
I S R P L K V L L T V V I V F I

GTCACTCAAC TGCCTTATAA CATTGTCAAG TTCTGCCGAG CCATAGACAT 800
V T Q L P Y N I V K F C R A I D I

CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG 850
I Y S L I T S C N M S K R M D I A

CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA 900
I Q V T E S I A L F H S C L N P

ATCCTTTATG TTTTTATGGG AGCATCTTTC AAAAACTACG TTATGAAAGT 950
I L Y V F M G A S F K N Y V M K V

GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT 1000
A K K Y G S W R R Q R Q S V E E F

TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT 1050
P F D S E G P T E P T S T F S I

TAAAGGTAAA ACTGCTCTGC CTTTTGCTTG GATACATATG AATGATGCTT 1100
- R - N C S A F C L D T Y E - C F

TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAAAAA AAAAAAM 1147
P L K N I C L I L K K K K K

FIG. 1

```
CCX-CKR          MALEQNQSTDYYYE--ENEMNGTY-------DYSQYELICIK   33
CCR9        MTPTDFTSPIPNMADDYG-SESTSSM-EDYVN----FNFTDF--YCEK
CCR7       MDLGKPMKSVLVVALLVIFQVCLCQDEVTDDYIGDNTTVDYTLFESLCSK
CCR6        MSGESMNFSDVFDSSEDYFVS-----VNTSYYS----VDSEML--LCSL
STRL33             MAEHDYHEDYGFS--------SF-NDSSQEEHQDF--L---

                             TM1
CCX-CKR    EDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKKQRTKTDVYILNL   83
CCR9       NNVRQFASHFLPPLYWLVFIVGALGNSLVILVYWYCTRVKTMTDMFLLNL
CCR7       KDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDTYLLNL
CCR6       QEVRQFSRLFVPIAYSLICVFGLLGNILVVITFAFYKKARSMTDVYLLNM
STRL33     ----QFSKVFLPCMYLVVFVCGLVGNSLMLVISIFYHKLQSLTDVFLVNL

                TM2                                TM3
CCX-CKR    AVADLLLLFTLPFWAV-NAVHGWVLGKIMCKITSALYTLNFVSGMQFLAC  132
CCR9       AIADLLFLVTLPFWAIA-AADQWKFQTFMCKVVNSMYKMNFYSCVLLIMC
CCR7       AVADILFLLTLPFWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLC
CCR6       AIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGMLLLTC
STRL33     PLADLVFVCTLPFWAYA-GIHEWVFGQVMCKSLLGIYTINFYTSMLILTC

                                        TM4
CCX-CKR    ISIDRYVAVTK-VPSQSGVGKP---CWIICFCVWMAAILLSIPQLVFYTV  178
CCR9       ISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQI
CCR7       ISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDL
CCR6       ISMDRYIAIVQATKSFRLRSRTLPRTKIICLVVWGLSVIISSSTFVFNQK
STRL33     ITVDRFIVVVKATKAYNQQAKRMTWGKVTSLLIWVISLLVSLPQIIYGNV

                                               TM5
CCX-CKR    NDNAR---CIPIFPRY-LGTSMKALIQMLEICIGFVVPFLIMGVCYFITA  224
CCR9       KEESGIAICTMVYPS-DESTKLKSAVLTLKVILGFFLPFVVMACCYTIII
CCR7       QRSSSEQAMRCSLIT-EHVEAF-ITIQVAQMVIGFLVPLLAMSFCYLVII
CCR6       YNTQGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIV
STRL33     FNLDKL-IC--GYH--DEAIS--TVVLATQMTLGFFLPLLTMIVCYSVII

                                   TM6
CCX-CKR    RTLMKMPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITS  274
CCR9       HTLIQAKKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISN
CCR7       RTLLQARNFERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSST
CCR6       KTLVQAQNSKRHKAIRVIIAVVLVFLACQIPHNMVLLV-TAANLGKMNRS
STRL33     KTLLHAGGFQKHRSLKIIFLVMAVFLLTQMPFNLMKFIRSTH------WE
```

FIG. 2A

```
                                   TM7
CCX-CKR    CNMSKRMDIAIQVTESIALFHSCLNPILYVFMGASFKNYVMK-------V 317
CCR9       CAVSTNIDICFQVTQTIAFFHSCLNPVLYVFVGERFRRDLVKTLKNLGCI
CCR7       CELSKQLNIAYDVTYSLACVRCCVNPFLYAFIGVKFRNDIFKLFKDLGCL
CCR6       CQSEKLIGYTKTVTEVLAFLHCCLNPVLYAFIGQKFRNYFLKILKDLWCV
STRL33     YYAMTSFHYTIMVTEAIAYLRACLNPVLYAFVSLKFRKNFWKLVKDIGCL

CCX-CKR    AKKY--GSWRRQRQSVEEFPFDSEGP--TEPTSTFSI              350
CCR9       SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL
CCR7       SQE-QLRQWSS----CRHIRR-SSMSVEAETTTTFSP
CCR6       RRKYKSSGFSCAGRYSENISRQTSETADNDNASSFTM
STRL33     P--Y--LGVSHQWKSSEDNSKTFSASHNVEATSMFQL
```

FIG. 2A
(CONTINUED)

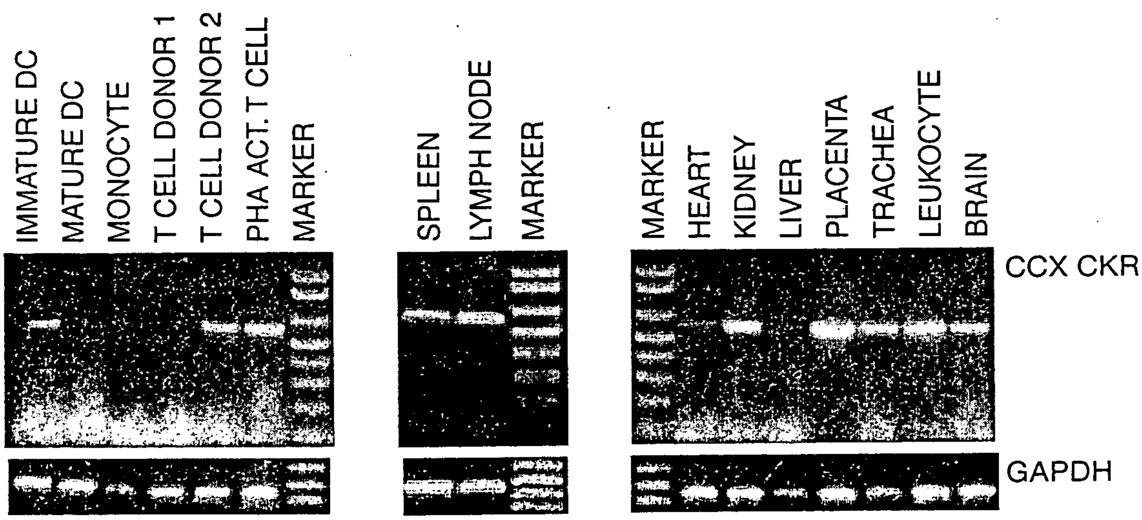


FIG. 2B

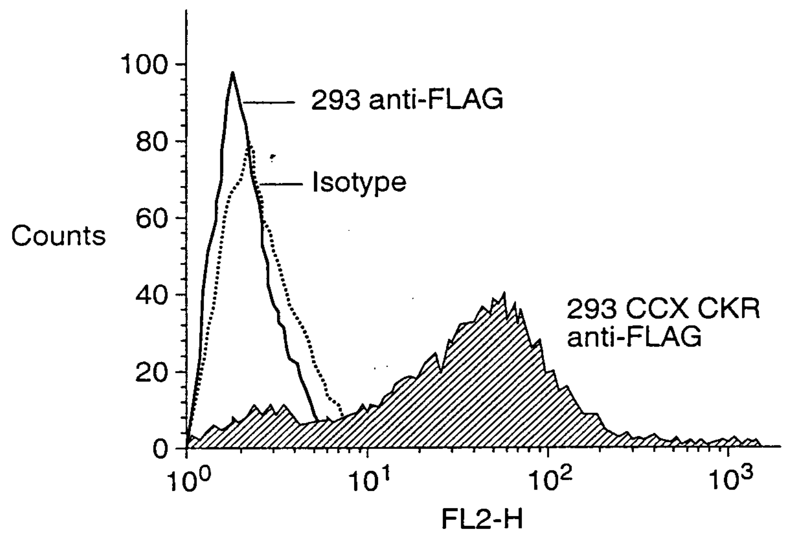

100
80
60
40
20
0
Counts
293 anti-FLAG
Isotype
293 CCX CKR
anti-FLAG
10^0
10^1
10^2
10^3
FL2-H

FIG. 2C

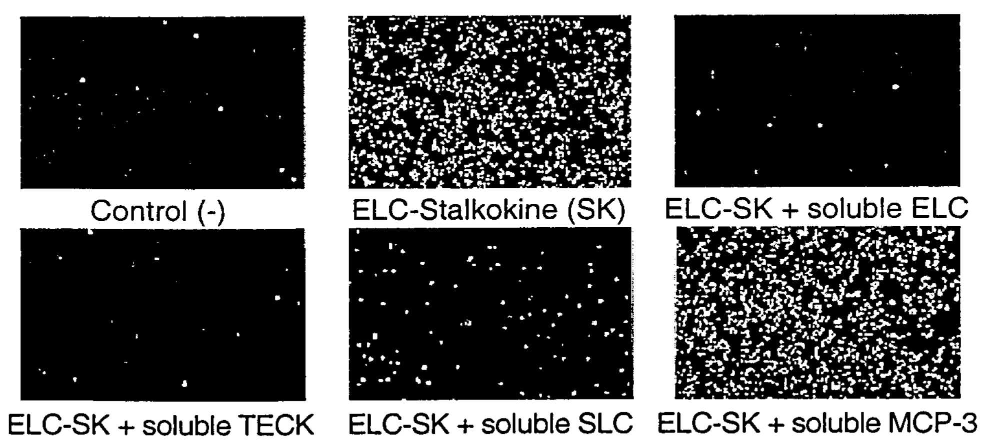

Control (-)
ELC-Stalkokine (SK)
ELC-SK + soluble ELC
ELC-SK + soluble TECK
ELC-SK + soluble SLC
ELC-SK + soluble MCP-3

FIG. 3A

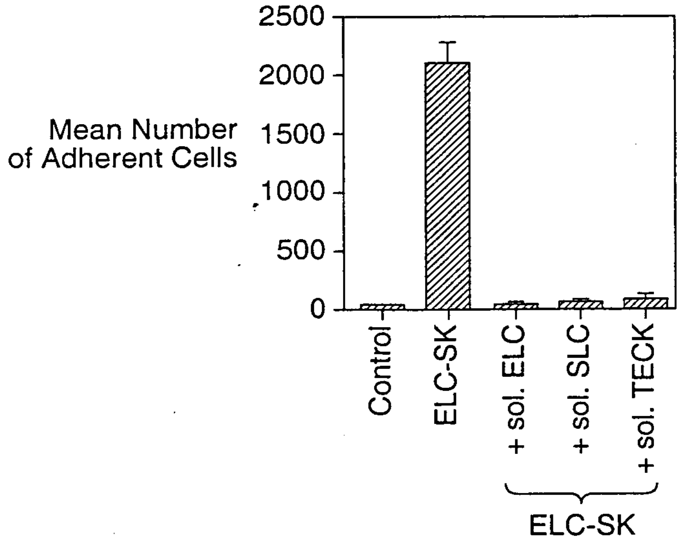

2500
2000
1500
1000
500
0
Mean Number
of Adherent Cells
Control
ELC-SK
+ sol. ELC
+ sol. SLC
+ sol. TECK
ELC-SK

FIG. 3B

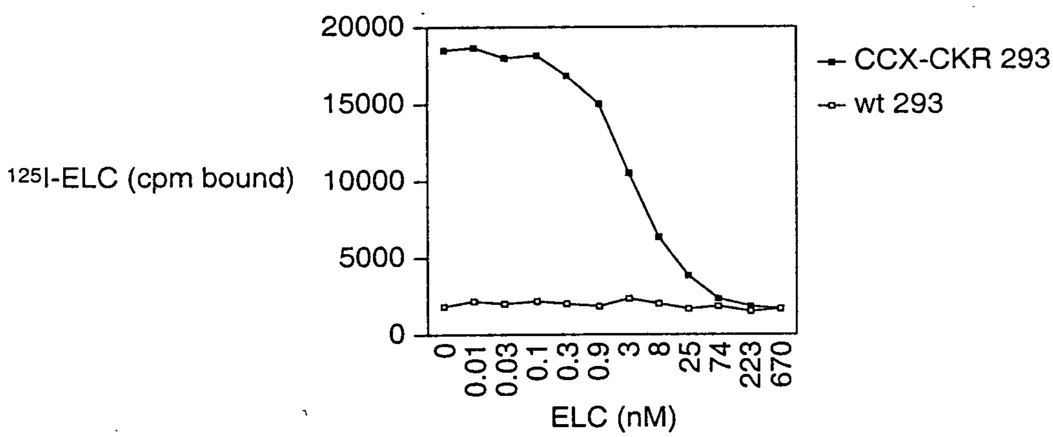

20000
15000
10000
5000
0
125I-ELC (cpm bound)
CCX-CKR 293
wt 293
0
0.01
0.03
0.1
0.3
0.9
3
8
25
74
223
670
ELC (nM)

FIG. 3C

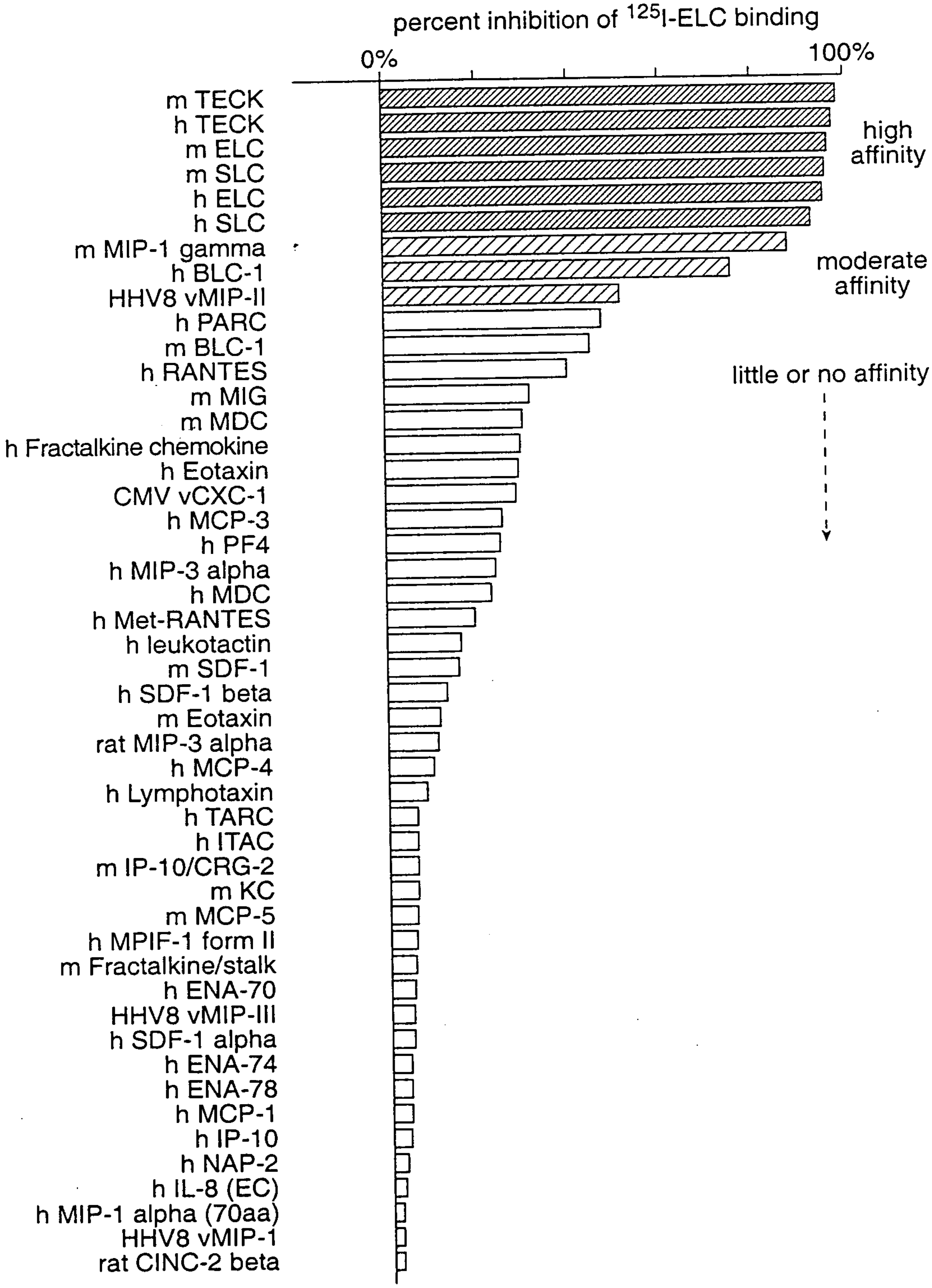

percent inhibition of 125I-ELC binding
0%
100%
high affinity
moderate affinity
little or no affinity
m TECK
h TECK
m ELC
m SLC
h ELC
h SLC
m MIP-1 gamma
h BLC-1
HHV8 vMIP-II
h PARC
m BLC-1
h RANTES
m MIG
m MDC
h Fractalkine chemokine
h Eotaxin
CMV vCXC-1
h MCP-3
h PF4
h MIP-3 alpha
h MDC
h Met-RANTES
h leukotactin
m SDF-1
h SDF-1 beta
m Eotaxin
rat MIP-3 alpha
h MCP-4
h Lymphotaxin
h TARC
h ITAC
m IP-10/CRG-2
m KC
m MCP-5
h MPIF-1 form II
m Fractalkine/stalk
h ENA-70
HHV8 vMIP-III
h SDF-1 alpha
h ENA-74
h ENA-78
h MCP-1
h IP-10
h NAP-2
h IL-8 (EC)
h MIP-1 alpha (70aa)
HHV8 vMIP-1
rat CINC-2 beta

FIG. 4A

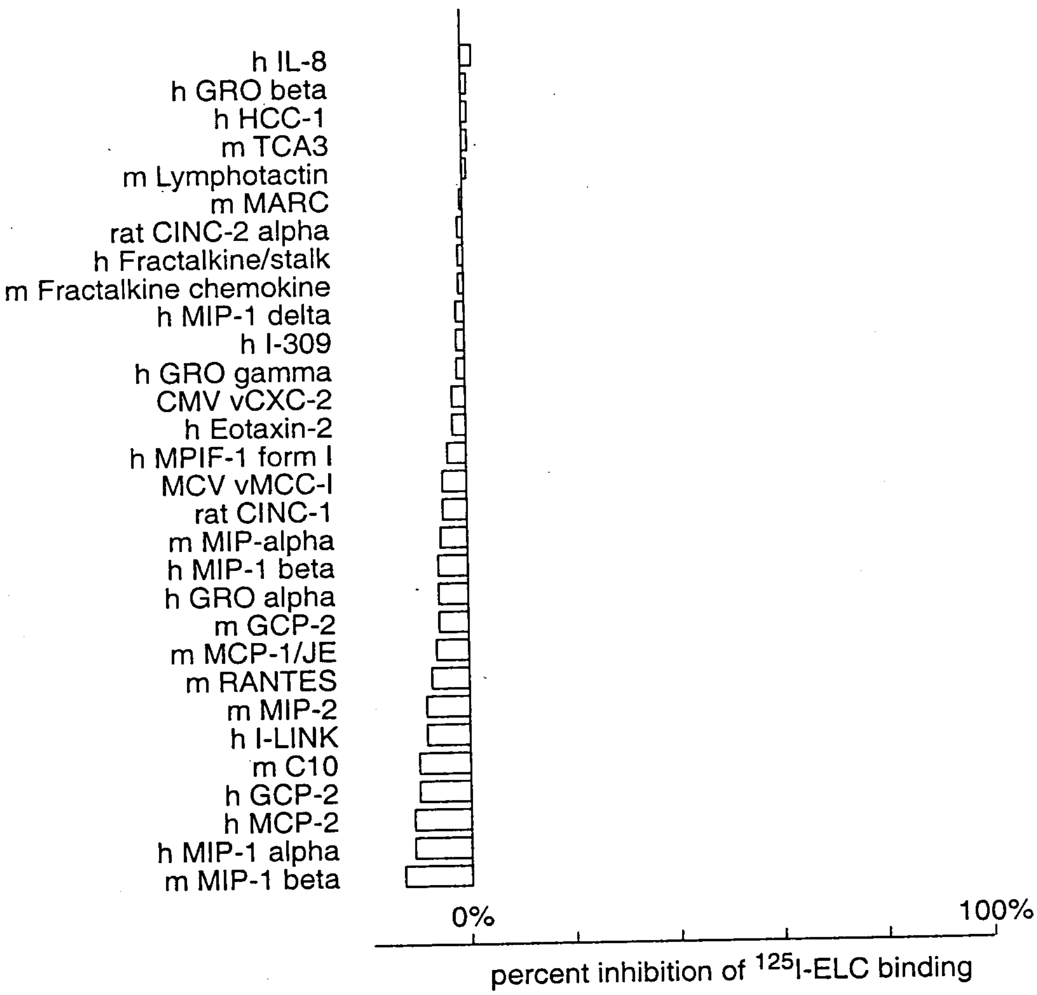
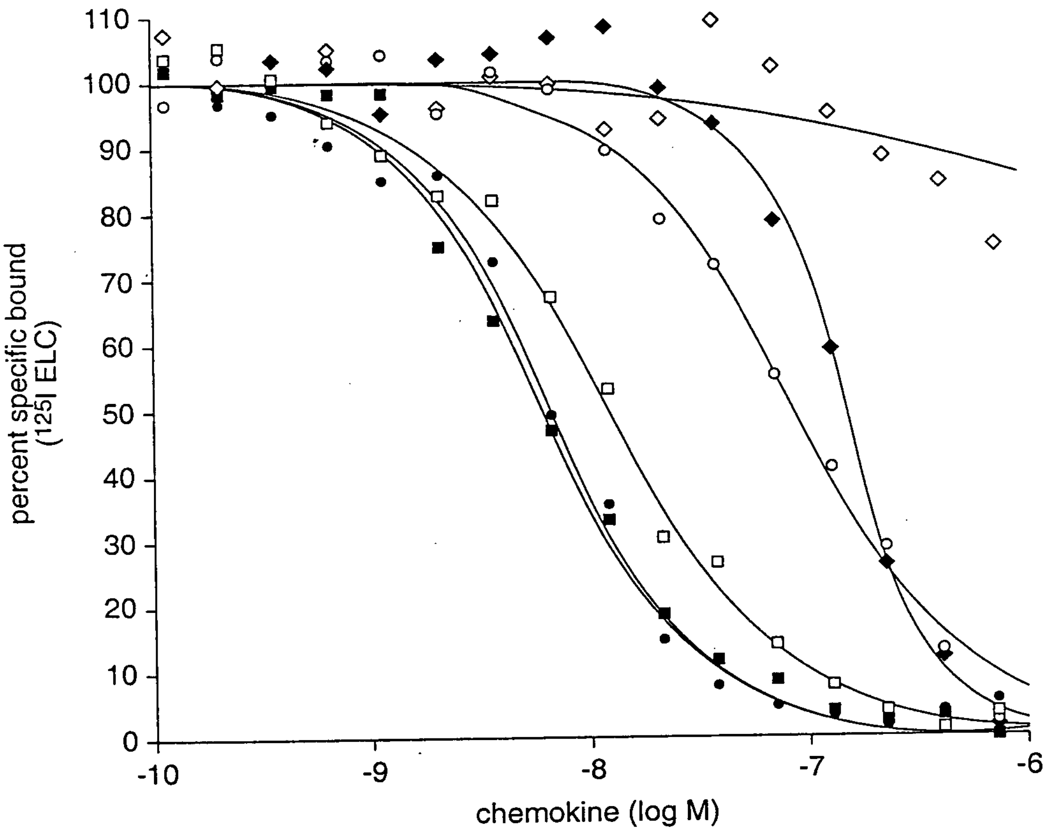


FIG. 4A
(CONTINUED)



human chemokines	IC-50	murine chemokines	IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

```
5'upstream   ATGCAGCATC TCGTTTATAA AAGGCAACTA GTGAAATTTA GTGCAAATGC  50
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   TGAGAGAATT TATTTAACTT ATTTAAATTA AATTTATAAA TAACATCAAA 100
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   ATAAAAAATA AATTTAATTT AAATAAACCA AGTAATTTGC TATTTTCGTT 150
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   TTTATTCAAT TTGTTGTAGA TATACTTTTA CGATTCACAA AATTATGTAT 200
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   GTAAAGATTA TAACACTATT TATTCTTTTT AGTTAAAATC TAATTAAATT 250
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   TTCATATTTT AAAAATCATT TTTACATAAA AGTCTTCACT TTTATTTAGG 300
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   ATTTAATGAT TAAGAAAATT CTCCAGGGCA TTATGTTTAT TGTCCTGTTC 350
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   AAATCCAAGC TCTTTCACAC AGAATTGTAC AAGCAAAGTT TGAGTAACTA 400
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   ATCTTGGGGT CATATTCCAA TGTGGCTCCC ATTAAAGCAT TTCAAAGAGT 450
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   GCTAGATTCA GGCTCACATA TGTTACAGCA ACAGGCTATA CTCTAGGGAA 500
CCXCKR       ---------- ---------- ---------- ---------- ----------

5'upstream   AGAACAAAAC AGCTTGATAG AAACTGTGTG CTTTTAAGCA TATTTAGACA 550
CCXCKR       ---------- ---------- ---------- ---------- ----------
                                  TRANSLATION START
5'upstream   AATATCTATC CTGTATTCTC TTTGCCATCT AGATTGGAGC CATGGCTTTG 600
CCXCKR       ---------- ---------- ---------- ---------- -ATGGCTTTG   9

5'upstream   GAACAGAACC -GTCAACAGA TTATTATTAT GAGGAGAAGT GAAATGAATG 649
CCXCKR       GAACAGAACC AGTCAACAGA TTATTATTAT GAGGA-AAAT GAAATGAATG  58

5'upstream   GC-CTGATGA CTACAGTCAG TATGAACTGA TCTGT----- --------TC 685
CCXCKR       GCACTTATGA CTACAGTCAA TATGAACTGA TCTGTATCAA AGAAGATGTC 108

5'upstream   AGAGAAGAGA CAGAGGATAT GC-ACAGGGT TGCTCCCTGT ATTGCTCACC 734
CCXCKR       AGAGAA---- -------TTT GCAAAAGTTT TCCTCCCTGT ATTCCTCACA 147

5'upstream   ATAG------ ---------- ---------- --------AG ---------- 740
CCXCKR       ATAGTTTTCG TCATTGGACT TGCAGGCAAT TCCATGGTAG TGGCAATTTA 197

5'upstream   ---------- ---------- ---------- ---------- ---------- 740
CCXCKR       TGCCTATTAC AAGAAACAGA GAACCAAAAC AGATGTGTAC ATCCTGAATT 247

5'upstream   ---------- ---------- ---------- ---------- ---------- 740
CCXCKR       TGGCTGTAGC AGATTTACTC CTTCTATTCA CTCTGCCTTT TTGGGCTGTT 297

5'upstream   ---------- ---------- ---------- ---------- ---------- 740
CCXCKR       AATGCAGTTC ATGGGTGGGT TTTAGGGAAA ATAATGTGCA AAATAACTTC 347
```

FIG. 5

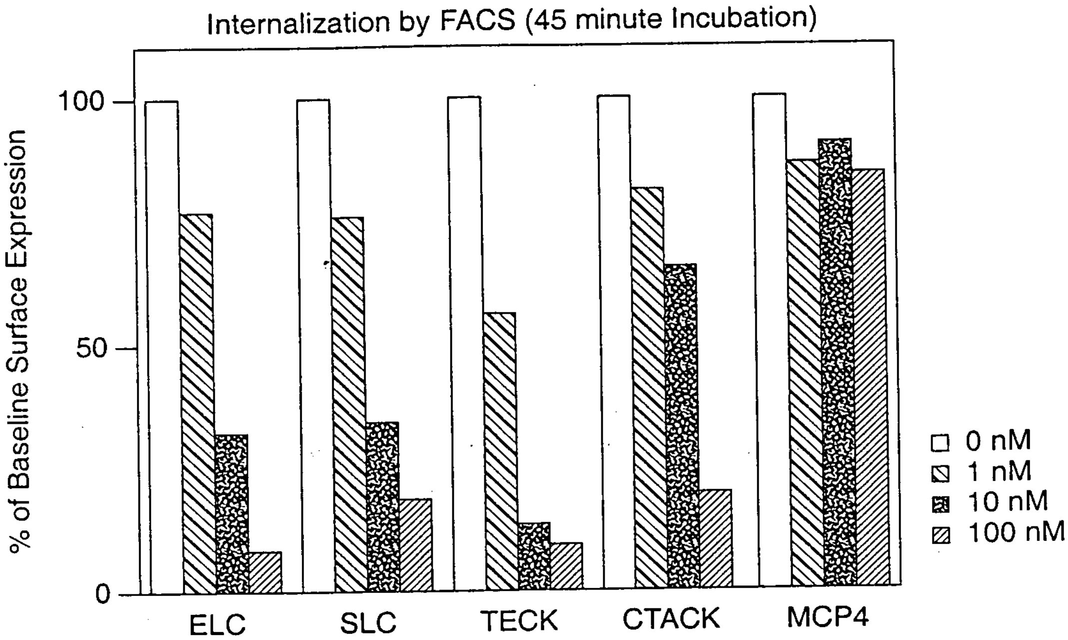

Internalization by FACS (45 minute Incubation)
100
50
0
% of Baseline Surface Expression
ELC
SLC
TECK
CTACK
MCP4
0 nM
1 nM
10 nM
100 nM

FIG. 6A

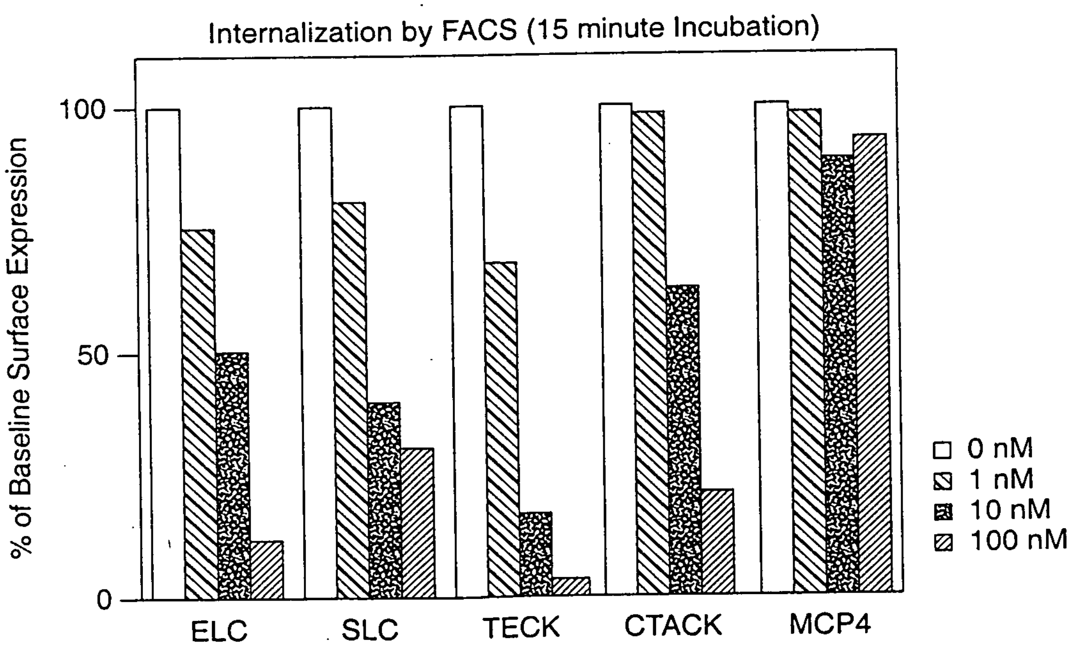

Internalization by FACS (15 minute Incubation)
100
50
0
% of Baseline Surface Expression
ELC
SLC
TECK
CTACK
MCP4
0 nM
1 nM
10 nM
100 nM

FIG. 6B